

identify as gay, bisexual, or are non-identified men who have sex with men (hereafter MSM). According to the CDC, Black MSM, with and without, CJI experience HIV incidences that exceed any other race/transmission group in the US. This systematic review focuses interventions that address epidemiologic risk factors associated with HIV and sexually transmitted infection (STI) in CJI populations and their potential relevance to Black MSM with CJI. We conducted electronic searches of Medline, PsycINFO, CINAHL, and the Cochrane Review of Clinical Trials databases. Studies published before January 1, 2017 that included over 30 Black men, HIV or STI as an outcome measure, and participants who were arrested, detained, or on parole/probation were included. Reviewers independently and systematically extracted and reviewed all studies using Downs and Black checklist for intervention studies. Authors cross-checked 20% of extractions for consistency, and used PRISMA guidelines for reporting findings. A total of 40 studies were included in the final analysis. Reporting on MSM as a distinct population was evident in just 36% of studies and subgroup analyses specific to Black MSM was rare. Interventions included HIV/STI education and screening, condom provision, linkage to HIV care and treatment, and mental health and substance misuse interventions. None of the interventions included biomedical HIV prevention (e.g., pre-exposure prophylaxis) beyond treatment as prevention. This analysis identifies both promising interventions for widescale adoption and key gaps in research on at-risk and HIV-infected CJI populations. Future research in CJI populations should allow for detailed subgroup analyses of Black MSM so that the effects on key health and social outcomes relevant to this highly impacted population are carefully assessed.

P67. Assessing Risk of Influenza Infection on a College Campus: An Emphasis on Housing Arrangement



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Background: Each year, millions of cases of influenza are reported in the United States. The virus can spread rapidly on college campuses, partially due to housing arrangements and social activities. The purpose of this study was to determine if housing arrangements were associated with increased influenza or influenza-like-illnesses (ILIs) infection rates at Liberty University.

Methods: Electronic surveys were administered and completed by 405 undergraduate and graduate students during October 2016. Data were analyzed to identify relative risk and assess correlation between housing arrangements and student illness. Geographic Information System (GIS) maps were created to display flu vaccination prevalence and self-reported flu symptoms by housing arrangement and location.

Results: Of the 405 participants 182 (44.9%) reported having an illness with flu-like symptoms. The residential annex had the highest rate of self-reported flu symptoms (56%) and commuter students had the lowest (40%). Of those surveyed 51 (12.6%) had received the 2016–2017 flu vaccination. The highest percentage of flu vaccination was in the Residential Annex (22%) and lowest in the Quads (0%). Risk of illness increased slightly with shared living spaces: bedroom (RR=1.06), bathroom (RR=1.19), kitchens (RR=1.03), and common spaces (RR=1.06). A Chi Square Test for Independence revealed no statistically significant relationship between housing arrangement and reported student illness ($p=0.68$, $\alpha=0.05$). A second Chi Square Test for Independence was run to determine if a relationship existed between class status and reported illness; again, no statistically significant relationship was found ($p=0.16$, $\alpha=0.05$).

Conclusions: The findings suggest that housing type has no statistically significant effect on the development of ILIs. Influenza vaccination rates were lower than the national average. However, they were still found to be a protective factor. Further studies should be conducted to better understanding how other risk factors contribute to influenza outbreaks on college campus and aid in development better public health interventions.

P68. Causal Variable Importance of Elixhauser Comorbidity Groups for In-hospital Mortality in Patients with Bloodstream Infection



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Purpose: The importance of the Elixhauser comorbidity system in patients who develop bloodstream infection (BSI) is uncertain. The purpose of this work was to quantify the contribution of Elixhauser comorbidity groups to in-hospital mortality in the population of patients who are diagnosed with BSI. **Methods:** We examined 4008 hospitalizations in 3495 patients (≥ 18 years old), who developed BSI at a 1250-bed tertiary-care center in St. Louis, Missouri, between 2011–2012. We identified a BSI case by a positive blood culture result with a known pathogen. We estimated a variable importance measure, population attributable fraction (AF_p), using targeted maximum likelihood estimation with super learning for a data-adaptive estimation of AF_p , which is defined as the fraction of all in-hospital mortality that would not have occurred if a specific comorbidity group had not existed.

Results: In-hospital mortality occurred in 16% of patients who developed BSI. Estimates of AF_p identified comorbidity groups that significantly contributed to in-hospital mortality after controlling for demographics and all other comorbidity groups, which included cardiac arrhythmias ($AF_p = 0.0259$), neurological disorders ($AF_p = 0.0195$), liver disease ($AF_p = 0.0247$), coagulopathy ($AF_p = 0.0185$), and fluid and electrolyte disorders ($AF_p = 0.0368$).

Conclusions: Several Elixhauser comorbidity groups are significantly contributing to in-hospital mortality in the population of patients diagnosed with BSI.

P69. Predicting Incidence of Norovirus Epidemiology in Oyster Harvesting Areas along Louisiana Gulf Coast



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Purpose: Tools for prediction of viral pathogens are crucial for securing the public health from risks of the associated illnesses. Norovirus (family Calciviridae) is the leading cause of epidemic gastroenteritis and outbreaks that frequently detected in oysters harvested from sewage-contaminated waters. A key priority in addressing the ongoing risk of norovirus outbreaks is identifying the environmental predictors and conditions controlling epidemics in coastal waters. The objective of this study is to apply machine learning techniques first to determine environmental factors governing outbreaks and then to develop prediction models for Louisiana Coast, which is highly prone to epidemics.

Method: Environmental data, along with various combinations of the explanatory variables were analyzed through Random Forests (RF) method to select final model input variables. The genetic programming (GP) algorithm was further used to predict norovirus outbreaks. Furthermore, the importance of the input variables to the model output was evaluated by global sensitivity analysis.

Result: Findings indicated that gage height, water temperature, and solar radiation were the most sensitive parameters influencing norovirus outbreaks, respectively. Moreover, GP managed successfully to predict norovirus outbreaks in the study area with the reasonable accuracy.

Conclusion: The machine learning approach, presented in this study, provided reliable tools for predicting potential norovirus outbreaks and preventing or at least reducing risks to the human health. This work contributes to the growing body of literature on norovirus epidemiology in terms of source, sink, and predictors.

Methods

P70. Peer-Reviewed Manuscript to Infographic: The Millennium Cohort Program's Method for Disseminating Evidence-Based Research



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Purpose: The Millennium Cohort Program, consisting of both the largest longitudinal cohort of U.S. Service members and a dyadic cohort of Service